

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/445,614DATE: 04/06/2001  
TIME: 10:45:39Input Set : A:\T1481.txt  
Output Set: N:\CRF3\04062001\I445614.raw

ENTERED

4 <110> APPLICANT: Bonnert, Timothy Peter  
6 <120> TITLE OF INVENTION: HUMAN VANILLOID RECEPTOR-LIKE RECEPTOR  
9 <130> FILE REFERENCE: T1481  
11 <140> CURRENT APPLICATION NUMBER: 09/445,614  
12 <141> CURRENT FILING DATE: 1999-12-08  
14 <150> PRIOR APPLICATION NUMBER: 9827016.8  
15 <151> PRIOR FILING DATE: 1998-12-08  
17 <160> NUMBER OF SEQ ID NOS: 19  
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
21 <210> SEQ ID NO: 1  
22 <211> LENGTH: 2469  
23 <212> TYPE: DNA  
24 <213> ORGANISM: Homo sapiens  
26 <400> SEQUENCE: 1  
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28 ggtcctggct ggaccgagca gcctccctcct ccttagatga cctcacccctc cagctctcca 120  
29 gtttcaggt tggagacatt agatggaggc caagaagatg gctctgaggc ggacagagga 180  
30 aagctggatt ttgggagccg gtcgcctccc atggagtac agttccaggcg cgaggaccgg 240  
31 aaattcgccc ctcagataag agtcaacctc aactaccgaa agggAACAGG tgccagttag 300  
32 ccggatccaa accgatttga ccgagatccg ctcttcaatg cggctccccg gggtgtcccc 360  
33 gaggatctgg ctggacttcc agagtaacct agcaagacca gcaagtaactt caccgactcg 420  
34 gaatacacag agggctccac aggttaagacg tgcctgatga aggctgtgtt gaaaccttaag 480  
35 gacggagtca atgcctgcat tctgccactg ctgcagatcg acaggactc tggcaatcc 540  
36 cagcccttgg taaatgcccgtt gtgcacagat gactattacc gaggccacag cgctctgcac 600  
37 atcgccattt agaagaggag totgcagtgt gtgaagctcc tgggtggagaa tggggccaat 660  
38 gtgcatttccc gggcctgccc ccgttcttc cagaaggcc aaggacttgc tttttatttc 720  
39 ggtgagctac ccctctcttt ggccgcttgc accaaggactt gggatgtgtt aagctaccc 780  
40 ctggagaacc cacaccagcc cgccagccctg caggccactg actcccaaggca acacacatgc 840  
41 ctgcatttccc tagtgatgtat ctcggacaac tcagctgaga acattgcact ggtgaccaggc 900  
42 atgtatgtat ggctccctcca agctggggcc cgcctctgcc ctaccgtgca gcttgaggac 960  
43 atccgcatttcc tgcaggatct cacgcctctg aagctggccg ccaaggaggca agatcgag 1020  
44 attttcaggc acatccgtca gggggagttt tcaggactga gccacccttc ccggaaatgtt 1080  
45 accgagtggc gctatggggcc ttccgggtt tcgctgtatg acctggcttc tgtgacagc 1140  
46 tgtgaggaga actcagtgtt ggagatcatt gccttcatc gcaagagccc gcaccgacac 1200  
47 cgaatggtcg ttttggagcc cctgaacaaa ctgctgcagg cggaaatggca tctgcctcatc 1260  
48 cccaaatctt tcttaaactt cctgtgtat ctgatctaca tggatcatctt caccgctgtt 1320  
49 ggcattaccat agcctaccct gaagaagcag gcccggccctc acctgaaagc ggagggttgg 1380  
50 aactccatgc tgctgacggg ccacatccctt atccctgtatg gggggatcta cctccctgt 1440  
51 ggccagctgt ggtacttctg gccggccac gtgttcatct gatctcgtt catagacagc 1500  
52 tactttggaaa tcctcttcc tttccaggcc ctgctcacag tgggtgtccca ggtgtgtgt 1560  
53 ttcctggcca tcgagtggtt cctggccctt cttgtgtctg cgctgggtgtt gggctggctg 1620  
54 aacctgtttt actatacag tggcttccag cacacaggca tctacagtgtt catgatccag 1680  
55 aaggtcatcc tgcgggaccc gtcgccttc cttctgtatctt acttagtctt cctttccggc 1740  
56 ttgcgtgtat ccctgggtt gctgagccag gaggcttggc gcccggccaa tcctacagggc 1800  
57 cccaaatgcca cagagtcaatg gcaagccatg gaggacagg aggacgaggca acacggggcc 1860  
58 cagtagggatggat gttatccatc agcctccctt gagctttca aattcaccat cggcatgggc 1920  
59 gagctggccct tccaggagca gtcgcacttc cggccatgg tgctgtgtt gctgtggcc 1980

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60	tacgtgctgc	tcacctacat	cctgctgctc	aacatgctca	tcgcccctcat	gagcgagacc	2040									
61	gtcaacagtg	tcgccactga	cagctggagc	atctggaagc	tgcagaaaagc	catctctgtc	2100									
62	ctggagatgg	agaatggcta	ttgggtgtgc	aggaagaagc	agcggggcagg	tgtgtatgtc	2160									
63	accgttggca	ctaagccaga	tggcagcccg	gatgagcgct	gtgtgttcag	ggtggaggag	2220									
64	gtgaactggg	cttcatggga	gcagacgctg	cctacgctgt	gtgaggacc	gtcagggggca	2280									
65	ggtgtccctc	gaactctcga	gaaccctgtc	ctggcttccc	ctccccaaaga	ggatgaggat	2340									
66	ggtgcctctg	aggaaaacta	tgtgcccgtc	cagctctcc	agtccaactg	atggcccaga	2400									
67	tgcagcagga	ggccagagga	cagagcagag	gatcttcca	accacatctg	ctggctctgg	2460									
68	ggtcccagt						2469									
70	<210>	SEQ ID NO:	2													
71	<211>	LENGTH:	824													
72	<212>	TYPE:	PRT													
73	<213>	ORGANISM:	Homo sapiens													
75	<400>	SEQUENCE:	2													
76	Met	Thr	Ser	Pro	Ser	Ser	Pro	Val	Phe	Arg	Ile	Glu	Thr	Leu	Asp	
77	1			5			10				15					
78	Gly	Gly	Gln	Glu	Asp	Gly	Ser	Glu	Ala	Asp	Arg	Gly	Lys	Leu	Asp	Phe
79				20			25				30					
80	Gly	Ser	Gly	Leu	Pro	Pro	Met	Glu	Ser	Gln	Phe	Gln	Gly	Glu	Asp	Arg
81				35			40				45					
82	Lys	Phe	Ala	Pro	Gln	Ile	Arg	Val	Asn	Ieu	Asn	Tyr	Arg	Lys	Gly	Thr
83				50			55				60					
84	Gly	Ala	Ser	Gln	Pro	Asp	Pro	Asn	Arg	Phe	Asp	Arg	Asp	Arg	Leu	Phe
85	65			65			70				75				80	
86	Asn	Ala	Val	Ser	Arg	Gly	Val	Pro	Gly	Ala	Gly	Gly	Ala	Thr	Cys	Thr
87				85			90				95					
88	Gly	Gly	Cys	Thr	Gly	Gly	Ala	Cys	Thr	Thr	Cys	Cys	Ala	Gly	Ala	Gly
89				100			105				110					
90	Thr	Ala	Cys	Cys	Thr	Gly	Ala	Gly	Cys	Ala	Ala	Gly	Ala	Cys	Cys	Ala
91				115			120				125					
92	Gly	Cys	Ala	Ala	Gly	Thr	Ala	Cys	Cys	Thr	Cys	Ala	Cys	Cys	Gly	Ala
93				130			135				140					
94	Cys	Thr	Cys	Gly	Glu	Asp	Leu	Ala	Gly	Leu	Pro	Glu	Tyr	Leu	Ser	Lys
95	145			145			150				155				160	
96	Thr	Ser	Lys	Tyr	Leu	Thr	Asp	Ser	Glu	Tyr	Thr	Glu	Gly	Ser	Thr	Gly
97				165			170				175					
98	Lys	Thr	Cys	Leu	Met	Lys	Ala	Val	Ieu	Asn	Ieu	Lys	Asp	Gly	Val	Asn
99				180			185				190					
100	Ala	Cys	Ile	Leu	Pro	Leu	Leu	Gln	Ile	Asp	Arg	Asp	Ser	Gly	Asn	Pro
101				195			200				205					
102	Gln	Pro	Leu	Val	Asn	Ala	Gln	Cys	Thr	Asp	Asp	Tyr	Tyr	Arg	Gly	His
103				210			215				220					
104	Ser	Ala	Leu	His	Ile	Ala	Ile	Glu	Lys	Arg	Ser	Ieu	Gln	Cys	Val	Lys
105	225			225			230				235				240	
106	Leu	Leu	Val	Glu	Asn	Gly	Ala	Asn	Val	His	Ala	Arg	Ala	Cys	Gly	Arg
107				245			250				255					
108	Phe	Phe	Gln	Lys	Gly	Gln	Gly	Thr	Cys	Phe	Tyr	Phe	Gly	Glu	Ieu	Pro
109				260			265				270					
110	Leu	Ser	Leu	Ala	Ala	Cys	Thr	Lys	Gln	Trp	Asp	Val	Val	Ser	Tyr	Ieu

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111	275	280	285
112	Leu Glu Asn Pro His Gln Pro Ala Ser Leu Gln Ala Thr Asp Ser Gln		
113	290	295	300
114	Gly Asn Thr Val Leu His Ala Leu Val Met Ile Ser Asp Asn Ser Ala		
115	305	310	315
116	Glu Asn Ile Ala Leu Val Thr Ser Met Tyr Asp Gly Leu Leu Gln Ala		320
117	325	330	335
118	Gly Ala Arg Leu Cys Pro Thr Val Gln Leu Glu Asp Ile Arg Asn Leu		
119	340	345	350
120	Gln Asp Leu Thr Pro Leu Lys Leu Ala Ala Lys Glu Gly Lys Ile Glu		
121	355	360	365
122	Ile Phe Arg His Ile Leu Gln Arg Glu Phe Ser Gly Leu Ser His Leu		
123	370	375	380
124	Ser Arg Lys Phe Thr Glu Trp Cys Tyr Gly Pro Val Arg Val Ser Leu		
125	385	390	395
126	Tyr Asp Leu Ala Ser Val Asp Ser Cys Glu Glu Asn Ser Val Leu Glu		
127	405	410	415
128	Ile Ile Ala Phe His Cys Lys Ser Pro His Arg His Arg Met Val Val		
129	420	425	430
130	Leu Glu Pro Leu Asn Lys Leu Leu Gln Ala Lys Trp Asp Leu Leu Ile		
131	435	440	445
132	Pro Lys Phe Phe Leu Asn Phe Leu Cys Asn Leu Ile Tyr Met Phe Ile		
133	450	455	460
134	Phe Thr Ala Val Ala Tyr His Gln Pro Thr Leu Lys Lys Gln Ala Ala		
135	465	470	475
136	Pro His Leu Lys Ala Glu Val Gly Asn Ser Met Leu Leu Thr Gly His		480
137	485	490	495
138	Ile Leu Ile Leu Leu Gly Gly Ile Tyr Leu Leu Val Gly Gln Leu Trp		
139	500	505	510
140	Tyr Phe Trp Arg Arg His Val Phe Ile Trp Ile Ser Phe Ile Asp Ser		
141	515	520	525
142	Tyr Phe Glu Ile Leu Phe Leu Phe Gln Ala Leu Leu Thr Val Val Ser		
143	530	535	540
144	Gln Val Leu Cys Phe Leu Ala Ile Glu Trp Tyr Leu Pro Leu Leu Val		
145	545	550	555
146	Ser Ala Leu Val Leu Gly Trp Leu Asn Leu Leu Tyr Tyr Thr Arg Gly		560
147	565	570	575
148	Phe Gln His Thr Gly Ile Tyr Ser Val Met Ile Gln Lys Val Ile Leu		
149	580	585	590
150	Arg Asp Leu Leu Arg Phe Leu Leu Ile Tyr Leu Val Phe Leu Phe Gly		
151	595	600	605
152	Phe Ala Val Ala Leu Val Ser Leu Ser Gln Glu Ala Trp Arg Pro Glu		
153	610	615	620
154	Ala Pro Thr Gly Pro Asn Ala Thr Glu Ser Val Gln Pro Met Glu Gly		
155	625	630	635
156	Gln Glu Asp Glu Gly Asn Gly Ala Gln Tyr Arg Gly Ile Leu Glu Ala		640
157	645	650	655
158	Ser Leu Glu Leu Phe Lys Phe Thr Ile Gly Met Gly Glu Leu Ala Phe		
159	660	665	670

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160 Gln Glu Gln Leu His Phe Arg Gly Met Val Leu Leu Leu Leu Ala  
 161 675 680 685  
 162 Tyr Val Leu Leu Thr Tyr Ile Leu Leu Leu Asn Met Leu Ile Ala Leu  
 163 690 695 700  
 164 Met Ser Glu Thr Val Asn Ser Val Ala Thr Asp Ser Trp Ser Ile Trp  
 165 705 710 715 720  
 166 Lys Leu Gln Lys Ala Ile Ser Val Leu Glu Met Glu Asn Gly Tyr Trp  
 167 725 730 735  
 168 Trp Cys Arg Lys Lys Gln Arg Ala Gly Val Met Leu Thr Val Gly Thr  
 169 740 745 750  
 170 Lys Pro Asp Gly Ser Pro Asp Glu Arg Trp Cys Phe Arg Val Glu Glu  
 171 755 760 765  
 172 Val Asn Trp Ala Ser Trp Glu Gln Thr Leu Pro Thr Leu Cys Glu Asp  
 173 770 775 780  
 174 Pro Ser Gly Ala Gly Val Pro Arg Thr Leu Glu Asn Pro Val Leu Ala  
 175 785 790 795 800  
 176 Ser Pro Pro Lys Glu Asp Glu Asp Gly Ala Ser Glu Glu Asn Tyr Val  
 177 805 810 815  
 178 Pro Val Gln Leu Leu Gln Ser Asn  
 179 820  
 181 <210> SEQ ID NO: 3  
 182 <211> LENGTH: 51  
 183 <212> TYPE: DNA  
 184 <213> ORGANISM: Artificial Sequence  
 186 <220> FEATURE:  
 187 <223> OTHER INFORMATION: Primer  
 189 <400> SEQUENCE: 3  
 190 tgttaccaat ctgaagtggg agcggccgcc tcatTTTT tttttttt t 51  
 192 <210> SEQ ID NO: 4  
 193 <211> LENGTH: 21  
 194 <212> TYPE: DNA  
 195 <213> ORGANISM: Artificial Sequence  
 197 <220> FEATURE:  
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 200 <400> SEQUENCE: 4  
 201 caggccccggg catgcacatt g 21  
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 204 <211> LENGTH: 21  
 205 <212> TYPE: DNA  
 206 <213> ORGANISM: Artificial Sequence  
 208 <220> FEATURE:  
 209 <223> OTHER INFORMATION: PCR Primer  
 211 <400> SEQUENCE: 5  
 212 ccagggcgag gaccggaaat t 21  
 214 <210> SEQ ID NO: 6  
 215 <211> LENGTH: 21  
 216 <212> TYPE: DNA  
 217 <213> ORGANISM: Artificial Sequence  
 219 <220> FEATURE:

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220 <223> OTHER INFORMATION: PCR Primer  
222 <400> SEQUENCE: 6  
223 gacagctgga gcatctggaa g 21  
225 <210> SEQ ID NO: 7  
226 <211> LENGTH: 21  
227 <212> TYPE: DNA  
228 <213> ORGANISM: Artificial Sequence  
230 <220> FEATURE:  
231 <223> OTHER INFORMATION: PCR Primer  
233 <400> SEQUENCE: 7  
234 gacagctgga gcatctggaa g 21  
236 <210> SEQ ID NO: 8  
237 <211> LENGTH: 21  
238 <212> TYPE: DNA  
239 <213> ORGANISM: Artificial Sequence  
241 <220> FEATURE:  
242 <223> OTHER INFORMATION: PCR Primer  
244 <400> SEQUENCE: 8  
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247 <210> SEQ ID NO: 9  
248 <211> LENGTH: 21  
249 <212> TYPE: DNA  
250 <213> ORGANISM: Artificial Sequence  
252 <220> FEATURE:  
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255 <400> SEQUENCE: 9  
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259 <211> LENGTH: 21  
260 <212> TYPE: DNA  
261 <213> ORGANISM: Artificial Sequence  
263 <220> FEATURE:  
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266 <400> SEQUENCE: 10  
267 ctctcttgg ccgcttgac c 21  
269 <210> SEQ ID NO: 11  
270 <211> LENGTH: 21  
271 <212> TYPE: DNA  
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280 <210> SEQ ID NO: 12  
281 <211> LENGTH: 21  
282 <212> TYPE: DNA  
283 <213> ORGANISM: Artificial Sequence  
285 <220> FEATURE:  
286 <223> OTHER INFORMATION: PCR Primer

**VERIFICATION SUMMARY**

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